New Disease Reports

First report of *Sugarcane streak mosaic virus* in sugarcane (*Saccharum* spp.) in Côte d'Ivoire

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Sugarcane streak mosaic virus (SCSMV) is a member of the genus *Poacevirus* (family *Potyviridae*) and is named for the pale green symptoms it causes on leaves of *Saccharum* sp. (sugarcane) (Figs. 1-2). SCSMV occurs in several Asian countries but has not been reported outside this continent (Chatenet *et al*., 2005; Damayanti & Putra 2011; Li *et al*., 2011). In 2016 streak mosaic symptoms were observed on the main sugarcane varieties at the Sucrivoire estate, Zuenoula, Côte d'Ivoire (Fig. 1). These symptoms were associated with a progressive decrease in sugar yield reaching 70% in 2017 in cv. R575. In October 2018 the symptoms were also found on at least one variety at the Sucaf Ferke2 estate, Ferkéssedougou (Fig. 2). In November and December 2018, surveys were conducted at the Ferke2 and Zuenoula estates, respectively. At Ferke2, symptoms were observed on all 11 commercially cultivated varieties with 0-25% stalks affected per field. Symptoms were also observed on 0- 15% plants per variety at plant cane stage 1 in nurseries with only two varieties, out of 16, showing no symptoms. The same disease symptoms were seen at Zuenoula where disease occurrence was higher than 95% in commercial fields and almost 100% in nurseries. One leaf from a symptom-bearing plant and one leaf from a symptomless plant were collected from each of 12 varieties grown in the Ferke2 nursery plot (Figs. 3-4). At a nursery in Zuenoula a symptom-bearing leaf from each of six varieties and one symptomless leaf from M2593/92, the only variety with symptomless plants, were sampled.

For molecular diagnosis, RNA and DNA were extracted from 100 mg of leaf tissue using RNeasy and DNeasy plant mini kits (Qiagen, Germany), respectively. Samples were screened for SCSMV using ST2 and ST5 primers (Chatenet *et al*., 2005), *Sugarcane mosaic virus* and *Sorghum mosaic virus* using oligo1n and oligo2n primers (Marie-Jeanne *et al*., 2000), and sugarcane-infecting streak viruses using SSV_1732F and SSV_2176R primers (Candresse *et al*., 2014). RNA and DNA viruses were amplified using the Qiagen one-step RT-PCR plant kit and the Promega GoTaq Hot Start Green Master Mix, respectively. A product of the expected size (400 bp) was obtained from 18 symptom-beairng but not from the 13 symptomless plants using ST2 and ST5 primers. All sugarcane samples tested negative for the other viruses. Amplicons from 16 symptom-bearing plants (6 from Zuenoula and 10 from Ferke2) were Sanger sequenced (Genewiz, USA) and the sequences were deposited in GenBank with Accession Nos. MK905373-MK905388. The trimmed sequences were each 343 nt long and shared 98.3-100% identity amongst each other. Thirteen of the 16 sequences had 99.7-100% identity with SCSMV isolate IND163 (AM502309.1) from India, while the three remaining sequences were very closely related to isolates IND159 (AM502305.1) and IND164 (AM502310.1) from India (99.1- 99.4% identity).

SCSMV appears to be responsible for the streak mosaic symptoms recently observed in Côte d'Ivoire, and virus isolates from Ferké2 and Zuenoula are highly related to SCSMV isolates from India. Streak mosaic is an important emerging disease of sugarcane in Côte d'Ivoire and affects a wide range of varieties, especially at Zuenoula where it appears to impact cane and sugar yields. To limit the impact of SCSMV, screening for SCSMV tolerance has been initiated in Ferké 2 (Pene & Behou 2019).

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Figure 1

Figure 2

Figure 3

Figure 4

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